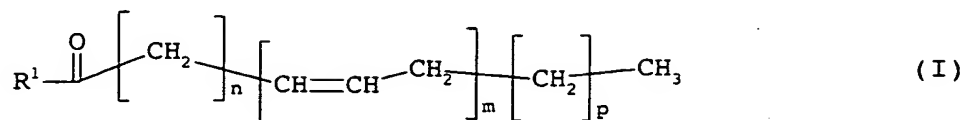


We claim:

1. A process for the production of compounds of the general
5 formula I:



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in transgenic plants with a content of at least 1% by weight
based on the total fatty acids, which process comprises the
15 following steps:

- a) introducing, into a plant, at least one nucleic acid
sequence which encodes a polypeptide with an
Δ6-desaturase activity; and
20 b) introducing at least one second nucleic acid sequence
which encodes a polypeptide with a Δ6-elongase activity;
and,
25 c) if appropriate, introducing a third nucleic acid sequence
which encodes a polypeptide with a Δ5-desaturase
activity;
d) followed by growing and harvesting the plants; and
30

where the variables and substituents in the formula I have
the following meanings:

35 $\text{R}^1 = -\text{OH}$, coenzyme A (thioester), phosphatidylcholine,
phosphatidylethanolamine, phosphatidylglycerol,
diphosphatidylglycerol, phosphatidylserine,
phosphatidylinositol, sphingolipid, glycosingolipid or a
radical of the following general formula II

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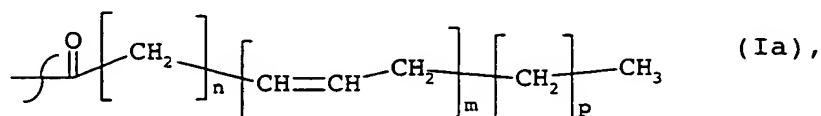
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R^2 = H, phosphatidylcholine-, phosphatidylethanolamine-,
 phosphatidylglycerol-, diphosphatidylglycerol-,
 phosphatidylserine-, phosphatidylinositol-, shingolipid-,
 glycoshingolipid-, glycoshingolipid- or saturated or
 5 unsaturated C_2 - C_{24} -alkylcarbonyl-,

R^3 = H, saturated or unsaturated C_2 - C_{24} -alkylcarbonyl-, or

R^2 and R^3 independently of one another represent a radical of
 10 the general formula Ia



$n = 3, 4$ or 6 , $m = 3, 4$ or 5 and $p = 0$ or 3 .

- 20 2. The process according to claim 1, wherein the substituents R^2 and R^3 independently of one another are C_{10} - C_{22} -alkylcarbonyl-.
3. The process according to claim 1 or 2, wherein the
 25 substituents R^2 and R^3 independently of one another are C_{16} -, C_{18} -, C_{20} - or C_{22} -alkylcarbonyl-.
4. The method according to any of claims 1 to 3, wherein the
 30 substituents R^2 and R^3 independently of one another are unsaturated C_{16} -, C_{18} -, C_{20} - or C_{22} -alkylcarbonyl- with one, two, three, four or five double bonds.
5. The method according to any of claims 1 to 4, wherein the
 35 transgenic plant is an oil crop.
6. The method according to any of claims 1 to 5, wherein the
 transgenic plant is selected from the group consisting of
 soya, peanut, oilseed rape, canola, linseed, evening
 primrose, verbascum, thistle, hazelnut, almond, macadamia,
 40 avocado, bay, wild roses, pumpkin/squash, pistachios, sesame,
 sunflower, safflower, borage, maize, poppy, mustard, hemp,
 castor-oil plant, olive, Calendula, Punica, oil palm, walnut
 or coconut.
7. The method according to any of claims 1 to 6, wherein the
 45 compounds of the formula I are obtained from the transgenic

plants in the form of their oils, fats, lipids or free fatty acids by pressing or extraction.

8. The process according to any of claims 1 to 7, wherein the oils, fats, lipids or free fatty acids obtained as claimed in claim 7 are refined.
9. The process according to any of claims 1 to 8, wherein the saturated or unsaturated fatty acids present in the compounds of the formula I are liberated.
10. The method according to any of claims 1 to 9, wherein the saturated or unsaturated fatty acids are liberated by alkaline hydrolysis or enzymatic cleavage.
11. The method according to any of claims 1 to 10, wherein the compounds of the general formula I are present in the transgenic plant at a content of at least 5% by weight, based on the total fatty acids.
12. The process according to any of claims 1 to 11, wherein the nucleic acid sequences which encode the polypeptides with $\Delta 6$ -desaturase activity, $\Delta 6$ -elongase activity or $\Delta 5$ -desaturase activity are selected from the group consisting of:
- a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29 or SEQ ID NO: 31,
 - b) nucleic acid sequences which, owing to the degeneracy of the genetic code, are obtained by back translation of the amino acid sequences shown in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30 or SEQ ID NO: 32,
 - c) derivatives of the nucleic acid sequences shown in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29 or SEQ ID NO: 31 which encode polypeptides with the amino acid sequences shown in SEQ ID NO: 2, SEQ ID NO: 4,

SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12,
SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID
NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26,
SEQ ID NO: 28, SEQ ID NO: 30 or SEQ ID NO: 32 and which
5 have at least 50% homology at the amino acid level,
without the enzymatic activity of the polypeptide being
substantially reduced.

13. The process according to any of claims 1 to 12, wherein the
10 nucleic acid sequences as claimed in claim 8 are linked with
one or more regulatory signals in a nucleic acid construct.
14. The method according to any of claims 1 to 13, wherein the
15 nucleic acid construct comprises additional biosynthetic
genes of the fatty acid or lipid metabolism selected from the
group consisting of acyl-CoA dehydrogenase(s), acyl-ACP
[= acyl carrier protein] desaturase(s), acyl-ACP
thioesterase(s), fatty acid acyl transferase(s), fatty acid
synthase(s), fatty acid hydroxylase(s), acetyl-coenzyme A
20 carboxylase(s), acyl-coenzyme A oxidase(s), fatty acid
desaturase(s), fatty acid acetylenases, lipxygenases,
triacylglycerol lipases, allene oxide synthases,
hydroperoxide lyases or fatty acid elongase(s).

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